SEQUENCE LISTING



COPY

531

<110> Wake Forest University
 Bowden, Donald W.
 Dawson, Paul A.
 Fossey, Sallyanne C.

<120> GLUT 10: A NOVEL GLUCOSE TRANSPORTER IN THE TYPE 2 DIABETES LINKED REGION OF CHROMOSOME 20Q12-13.1

| REGION | OF CHROMOSOME | 20Q12-13.1 | · · | | |
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| qqqqac | teeg gegggggat | g cgcgcccggc co | ctcagcgc cc | ccagcacg ccgcc | gagtc 240 |
| 2333 | 5 5 55555 | | | • | • |
| cegete | gcc atg ggc ca Met Gly Hi 1 | c tec eca ect g s Ser Pro Pro V 5 | al Leu Pro | ttg tgt gcc to Leu Cys Ala Se 10 | t gtg 291 r Val |
| | | | | | |
| tct tt | g ctg ggt ggc | ctg acc ttt ggt | : tat gaa ct | tg gca gtc ata | tca 339 |
| Ser Le | u Leu Gly Gly | Leu Thr Phe Gly | / Tyr Glu Le | eu Ala Val Ile | Ser |
| 15 | • | 20 . | 25 | • | 30 |
| | | | | | |
| aat ac | c ctg ctg cca | ctg cag ctt gad | ttt gag ct | ta age tge ttg | gag 387 |
| GIV AI | a Leu Leu Pro | Leu Gln Leu Asp | Phe Glv Le | eu Ser Cvs Leu | Glu |
| 027 122 | 35 | , , | 40 | 45 | • |
| | , 33 | | .20 | | |
| | | | . ata aaa aa | nt ata ata asa | too ' 425 |
| cag ga | g tre erg grg | ggc agc ctg ctc | . ctg ggg gc | Le ten ten 33 | tcc 435 |
| Gln Gl | | Gly Ser Leu Leu | r ren era yr | | ser . |
| • | 50 | . 55 | | 60 | |
| | | | , | . • | • |
| ctg gt | t ggt ggc ttc | ctc att gac tgd | tať ggc ag | gg aag daa ged | atc 483 |
| Leu Va | l Gly Gly Phe | Leu Ile Asp Cys | Tyr Gly Ar | rg Lys Gln Ala | Ile · |
| | 65 | 70 | | 75 | |
| • | = = | | | | |

ctc ggg agc aac ttg gtg ctg ctg gca ggc agc ctg acc ctg ggc ctg

Leu Gly Ser Asn Leu Val Leu Leu Ala Gly Ser Leu Thr Leu Gly Leu

| 80 | 85 | 90 |
|----|----|----|
| | | |

| gct Ala 95 | ggt Gly | tcc Ser | ctg Leu | gcc Ala | tgg Trp 100 | ctg Leu | gtc Val | ctg Leu | ggc Gly | cgc Arg 105 | gct Ala | gtg Val | gtt Val | ggc | ttc Phe 110 | | 579 |
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| gcc Ala | att Ile | tcc Ser | ctc Leu | tcc Ser 115 | tcc Ser | atg Met | gct Ala | tgc Cys | tgt Cys 120 | atc Ile | tac Tyr | gtg Val | tca Ser | gag Glu 125 | ctg Leu | | <u>6</u> 27 |
| gtg Val | Gly ggg | cca Pro | cgg Arg 130 | cag Gln | cgg Arg | gga Gly | gtg Val | ctg Leu 135 | gtg Val | tcc Ser | ctc Leu | tat Tyr | gag Glu 140 | gca Ala | Gly | | 675 |
| atc Ile | acc Thr | gtg Val 145 | ggc | atc Ile | ctg Leu | ctc Leu | tcc Ser 150 | tat Tyr | gcc Ala | ctc Leu | aac Asn | tat Tyr 155 | gca Ala | ctg Leu | gct Ala | • | 723 |
| ggt Gly | acc Thr 160 | ccc Pro | tgg Trp | gga Gly | tgg Trp | agg Arg 165 | cac His | atg Met | ttc Phe | ggc | tgg Trp 170 | gcc Ala | act Thr | gca Ala | cct Pro | | 771 |
| gct Ala 175 | gtc Val | ctg Leu | caa Gln | tcc Ser | ctc Leu 180 | agc Ser | ctc Leu | ctc Leu | ttc Phe | ctc Leu 185 | cct Pro | gct Ala | ggt Gly | aca Thr | gat Asp 190 | | 819 |
| gag Glu | act Thr | gca Ala | aca Thr | cac His 195 | aag Lys | gac Asp | ctc Leu | atc Ile | cca Pro 200 | ctc Leu | cag Gln | gga Gly | ggt Gly | gag Glu 205 | gcc Ala | | 867 |
| ccc Pro | aag Lys | ctg Leu | ggc Gly 210 | ccg Pro | Gly aaa | agg Arg | cca Pro | cgg Arg 215 | tac Tyr | tcc Ser | ttt Phe | ctg Leu | gac Asp 220 | ctc Leu | ttc Phe | | 915 |
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| gtg Val | ctc Leu 240 | ttc Phe | cag Gln | caa Gln | cta Leu | aca Thr 245 | gly aaa | cag Gln | ccc Pro | aac Asn | gtg Val 250 | ctg Leu | tgc Cys | tat Tyr | gcc Ala | | 1011 |
| tcc Ser 255 | acc Thr | atc Ile | ttc Phe | agc Sèr | tcc Ser 260 | gtt Val | ggt Gly | ttc Phe | cat His | 999 Gly 265 | gga Gly | tcc Ser | tca Ser | gcc Ala | gtg Val 270 | • | 1059 |
| ctg Leu | gcc Ala | tct Ser | gtg Val | 999 Gly 275 | ctt Leu | Gly | gca Ala | gtg Val | aag Lys 280 | gtg Val | gca Ala | gct Ala | acc Thr | ctg Leu 285 | acc Thr | | 1107 |
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| ggc | tgt Cys | gcc Ala 305 | ctc Leu | atg Met | gcc Ala | ctg Leu | tcc Ser 310 | gtc Val | agt Ser | Gjy | ata Ile | .ggc Gly 315 | ctc Leu | gtc Val | agc Ser | - | 1203 |
| ttt Phe | gcc Ala 320 | Val | ccc Pro | atg Met | gac Asp | tca Ser 325 | Gly | cca Pro | agc | tgt Cys | ctg Leu 330 | Ala | gtg Val | ccc Pro | aat [°] Asn | | 1251 |

| gcc Ala 335 | acc Thr | GJA aaa | cag Gln | aca Thr | ggc Gly 340 | ctc Leu | cct Pro | gga Gly | gac Asp | tct Ser 345 | ggc Gly | ctg Leu | ctg Leu | cag Gln | gac Asp 350 | 1299 |
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| tcc Ser | tct Ser | cta Leu | cct Pro | ccc Pro 355 | att Ile | cca Pro | agg Arg | acc Thr | aat Asn 360 | gag Glu | gac Asp | caa Gln | agg Arg | gag Glu 365 | cca Pro | 1347 |
| atc Ile | ttg Leu | tcc Ser | act Thr 370 | gct Ala | aag Lys | aaa Lys | acc Thr | aag Lys 375 | ccc Pro | cat His | ccc Pro | aga Arg | tct Ser 380 | gga Gly | gac Asp | 1395 |
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| cct Pro | ctg Leu 400 | ccc Pro | gct Ala | cgg Arg | gly ggg | cat His 405 | gca Ala | ctg Leu | ctg Leu | cgc Arg | tgg Trp 410 | acc Thr | gca Ala | ctg Leu | ctg Leu | 1491 |
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| agc Ser | ctc Leu | tcc Ser 465 | ttc Phe | ctc Leu | gat Asp | ctc Leu | att Ile 470 | ggc | acc Thr | atc Ile | ggc | ttg Leu 475 | tcc Ser | tgg Trp | acc Thr | 1683 |
| ttc Phe | ctg Leu 480 | Leu | tac Tyr | gga Gly | ctg Leu | acc Thr 485 | gct Ala | gtc Val | ctc Leu | ggc Gly | ctg Leu 490 | ggc | ttc Phe | atc Ile | tat Tyr | 1731 |
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| Leu Leu Pro Leu Gln Leu Asp Phe Gly Leu Ser Cys Leu Glu Gln Glu 35 40 45 |
| Phe Leu Val Gly Ser Leu Leu Leu Gly Ala Leu Leu Ala Ser Leu Val 50 55 60 |
| Gly Gly Phe Leu Ile Asp Cys Tyr Gly Arg Lys Gln Ala Ile Leu Gly 65 70 75 80 |
| Ser Asn Leu Val Leu Leu Ala Gly Ser Leu Thr Leu Gly Leu Ala Gly 85 90 95 |
| Ser Leu Ala Trp Leu Val Leu Gly Arg Ala Val Val Gly Phe Ala Ile 100 105 110 |

Val Gly Ile Leu Leu Ser Tyr Ala Leu Asn Tyr Ala Leu Ala Gly Thr

Ser Leu Ser Ser Met Ala Cys Cys Ile Tyr Val Ser Glu Leu Val Gly

Pro Arg Gln Arg Gly Val Leu Val Ser Leu Tyr Glu Ala Gly Ile Thr

130 .

Pro Trp Gly Trp Arg His Met Phe Gly Trp Ala Thr Ala Pro Ala Val Leu Gln Ser Leu Ser Leu Leu Phe Leu Pro Ala Gly Thr Asp Glu Thr Ala Thr His Lys Asp Leu Ile Pro Leu Gln Gly Gly Glu Ala Pro Lys Leu Gly Pro Gly Arg Pro Arg Tyr Ser Phe Leu Asp Leu Phe Arg Ala Arg Asp Asn Met Arg Gly Arg Thr Thr Val Gly Leu Gly Leu Val Leu Phe Gln Gln Leu Thr Gly Gln Pro Asn Val Leu Cys Tyr Ala Ser Thr Ile Phe Ser Ser Val Gly Phe His Gly Gly Ser Ser Ala Val Leu Ala Ser Val Gly Leu Gly Ala Val Lys Val Ala Ala Thr Leu Thr Ala Met Gly Leu Val Asp Arg Ala Gly Arg Arg Ala Leu Leu Leu Ala Gly Cys Ala Leu Met Ala Leu Ser Val Ser Gly Ile Gly Leu Val Ser Phe Ala Val Pro Met Asp Ser Gly Pro Ser Cys Leu Ala Val Pro Asn Ala Thr Gly Gln Thr Gly Leu Pro Gly Asp Ser Gly Leu Leu Gln Asp Ser, Ser Leu Pro Pro Ile Pro Arg Thr Asn Glu Asp Gln Arg Glu Pro Ile Leu Ser Thr Ala Lys Lys Thr Lys Pro His Pro Arg Ser Gly Asp Pro Ser Ala Pro Pro Arg Leu Ala Leu Ser Ser Ala Leu Pro Gly Pro Pro Leu

Pro Ala Arg Gly His Ala Leu Leu Arg Trp Thr Ala Leu Leu Cys Leu 410 405 Met Val Phe Val Ser Ala Phe Ser Phe Gly Phe Gly Pro Val Thr Trp 425 420 Leu Val Leu Ser Glu Ile Tyr Pro Val Glu Ile Arg Gly Arg Ala Phe 440 Ala Phe Cys Asn Ser Phe Asn Trp Ala Ala Asn Leu Phe Ile Ser Leu 455 Ser Phe Leu Asp Leu Ile Gly Thr Ile Gly Leu Ser Trp Thr Phe Leu 475 470 Leu Tyr Gly Leu Thr Ala Val Leu Gly Leu Gly Phe Ile Tyr Leu Phe 485 490 Val Pro Glu Thr Lys Gly Gln Ser Leu Ala Glu Ile Asp Gln Gln Phe 505 Gln Lys Arg Arg Phe Thr Leu Ser Phe Gly His Arg Gln Asn Ser Thr 520 515 Gly Ile Pro Tyr Ser Arg Ile Glu Ile Ser Ala Ala Ser 530 535 <210> 3 <211> 20 <213> Artificial sequence <223> Synthetic oligonucleotide <400> 3 20 ggcacctctt ccctgcaaag <210> 4 <211> 20 <212> DNA <213> Artificial sequence <220> <223> Synthetic oligonucleotide . <400> 4 20

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